

SEQUENCE LISTING

<110> Crane, Edmund H. III
Rice, Douglas A.

<120> Maize NPR1 Polynucleotides and Methods
of Use

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<150> 60/130,692

<151> 1999-04-23

<150> 09/551,778

<151> 2000-04-18

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Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro	
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Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly	
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gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg	252
Gly Val Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu	
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aac cgg ctc agc aaa aac ctc gag cgg ctg ctc ctc gac ccg gac cta	300
Asn Arg Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu	
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gac tgc agc gac gcc gac gtc gat gtg ccc gac ggt ggg ccg ccc gta	348
Asp Cys Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val	
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Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala	
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gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg cgg	492
Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg	
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Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala	
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Phe Gln Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala	
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Pro Val Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser	
175 180 185 190	
tgc ccg ccg gcc atc agg tcc gcg gtc gag ctc atg tac gcg gcg tgt	684
Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys	
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acc ttc aag atc ccc gag ctc acc tcg ctc ttc cag cgc cgg ctt ctt	732
Thr Phe Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu	
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aat ttt gta gac aag act cta gtg gag gat gtt att cct att ctg gaa	780
Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu	
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Val Ala Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln	
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Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu	
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cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa	924
Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln	
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Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val	
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aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca	1068
Lys Leu Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala	
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tta cac tat gct gct tct tac tgt gat cct aaa gtt gtc tca gag ctg	1116
Leu His Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu	

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aca gca ctc cac ttg gct gct atg agg aga gaa cca gct ata atc atg				1212
Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met				
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tgt ctc ctt aac aaa ggg gca aat gtg tca caa ctg aca gct gat ggc				1260
Cys Leu Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly				
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agg agc gca att ggt att tgt cgg agg tta aca aga gca aaa gac tac				1308
Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr				
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Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys				
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Ile Asp Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu				
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gat gcc gtc acc tcg cct ttg ttg gca gat gat ctt cac atg aag ctt				1452
Asp Ala Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu				
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Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala				
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Glu Ala Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu				
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Phe Gly Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg				
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gag gtg gac ctt aat gag acg cca gtg aca caa aac aaa agg ctc cgt				1644
Glu Val Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg				
515		520	525	
tca agg gta gat gca ctg atg aaa aca gtg gag ctg ggc cgt cgg tac				1692
Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr				
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ttc ccg aac tgc tcg cag gtg ctg gac aag ttc ctg gag gac gat ctg				1740
Phe Pro Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu				
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ccg gaa ggt ctg gac cag ttc tac ctc cag agg ggc aca gcc gat gag				1788
Pro Glu Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu				
560		565	570	
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Gln Lys Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu				
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 Ser Ser Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
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 50 55 60
 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
 65 70 75 80
 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
 85 90 95
 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
 100 105 110
 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
 115 120 125
 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
 130 135 140
 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
 145 150 155 160
 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
 165 170 175
 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
 180 185 190
 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
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 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
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 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
 225 230 235 240
 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
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 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
 260 265 270
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 275 280 285
 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
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 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
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 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
 405 410 415
 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
 420 425 430
 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
 435 440 445
 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
 450 455 460
 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
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 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
 485 490 495
 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
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 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

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used for cDNA library construction and poly(dT) to
remove clones which have a poly(A) tail but no
cDNA insert.

<400> 6

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36

10047593 "011502"